

In silico genome wide analysis of aquaporins in *Musa acuminata*

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Abstract: Major intrinsic proteins (MIPs) involved in water and nutrient permeability are called aquaporins (AQPs). AQPs facilitate transport of water and molecules such as H₂O₂, CO₂, silicon, boron, urea, and ammonia. Crops with an enormous food and feed security role and trade potential are sensitive to any kind of water deficit. Transportation of solutes across membrane has vital role in plant normal physiology and resistance toward stresses. Fusarium wilt disease and Sigatoka leaf spots threaten global market of *Musa sp.* The aim of this study was to identify AQPs that are involved in the transportation of water and minerals by *in silico* genome wide analyses and evaluate their expression level under pathogen attack. After mining of the *AQP* coding genes of *Musa acuminata* from genomic databases and identification of trans-membrane helical domains, location of *MIP* genes on the chromosomes and localization of MIP proteins in the subcellular compartments have been determined [1]. The substrate selectivity of MIPs has been revealed by *in silico* analysis. Evolutionary analysis showed that *Musa* MIPs are classified into four distinct clusters, including plasma membrane intrinsic proteins (PIPs), tonoplast intrinsic proteins (TIPs), nodolin-26 like intrinsic proteins (NIPs), and small basic intrinsic proteins (SIPs) [1]. Since identification of MIPs which are influenced by stresses provides the opportunity for the production of transgenic resistant cultivars, digital expression level of *AQP* genes were downloaded from Gene Expression Omnibus and analyzed by the MeV 4.9 program. Expression level of MIPs was mainly suppressed by acetylene and biotic treatments [2]. Conclusively, suppression of *MIP* genes is in line with the repression of plant defense by pathogens as an approach for infection progression.

Keywords: Aquaporin; *Musa acuminata*; Evolution; Biotic stress; Expression profile

References

- [1] S. Hemmati, "Predicting the functionality of major intrinsic proteins: an *in silico* analysis in *Musa*," *TiPS.*, 2 (2016) 139-150.
- [2] S. Hemmati, "Analysis of the expression level of aquaporins under acetylene treatment and pathogen attack," *TiPS.*, 3 (2017) 71-82.